Package 'NanoMethViz'

March 4, 2021

Type Package

Title Visualise methlation data from Oxford Nanopore sequencing

Version 1.0.0

Description NanoMethViz is a toolkit for visualising methylation data from Oxford Nanopore sequencing. It can be used to explore methylation patterns from reads derived from Oxford Nanopore direct DNA sequencing with methylation called by callers including nanopolish, f5c and megalodon. The plots in this package allow the visualisation of methylation profiles aggregated over experimental groups and across classes of genomic features.

biocViews Software, Visualization, DifferentialMethylation

URL https://github.com/shians/NanoMethViz

BugReports https://github.com/Shians/NanoMethViz/issues

Depends R (>= 4.0.0), methods, ggplot2

Imports S4Vectors, SummarizedExperiment, bsseq, forcats, assertthat, AnnotationDbi, Rcpp, dplyr, data.table, e1071, fs, GenomicRanges, ggthemes, glue, patchwork, purrr, readr, rlang, RSQLite, Rsamtools, scales, stats, stringr, tibble, tidyr, utils, zlibbioc

Suggests DSS, Mus.musculus, Homo.sapiens, knitr, rmarkdown

LinkingTo Rcpp

License Apache License (>= 2.0)

SystemRequirements C++11

VignetteBuilder knitr

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

git_url https://git.bioconductor.org/packages/NanoMethViz

git_branch RELEASE_3_12

git_last_commit 60b2e12

git_last_commit_date 2020-10-27

Date/Publication 2021-03-03

Author Shian Su [cre, aut]

Maintainer Shian Su <su.s@wehi.edu.au>

R topics documented:

`bsseq_to_edger` *Convert BSseq object to edgeR methylation matrix*

Description

Convert BSseq object to edgeR methylation matrix

Usage

```
bsseq_to_edger(bsseq)
```

Arguments

`bsseq`	the BSseq object.

Value

a matrix compatible with the edgeR differential methylation pipeline

Examples

```
methy <- system.file("methy_subset.tsv.bgz", package = "NanoMethViz")
bsseq <- methy_to_bsseq(methy)
edger_mat <- bsseq_to_edger(bsseq)
```

bsseq_to_log_methy_ratio *Convert BSseq object to log-methylation-ratio matrix*

Description

Creates a log-methylation-ratio matrix from a BSseq object that is useful for dimensionality reduction plots.

Usage

```
bsseq_to_log_methy_ratio(bsseq, prior_count = 2)
```

Arguments

bsseq	the BSseq object.
prior_count	the prior count added to avoid taking log of 0.

Value

a matrix containing log-methylation-ratios.

Examples

```
methy <- system.file("methy_subset.tsv.bgz", package = "NanoMethViz")
bsseq <- methy_to_bsseq(methy)
log_m_ratio <- bsseq_to_log_methy_ratio(bsseq)
```

create_tabix_file *Create a tabix file using methylation calls*

Description

Create a tabix file using methylation calls

Usage

```
create_tabix_file(
  input_files,
  output_file,
  samples = extract_file_names(input_files),
  verbose = TRUE
)
```

Arguments

input_files	the files to convert
output_file	the output file to write results to (must end in .bgz)
samples	the names of samples corresponding to each file
verbose	TRUE if progress messages are to be printed

Value

invisibly returns the output file path, creates a tabix file (.bgz) and its index (.bgz.tbi)

Examples

```
methy_calls <- system.file(package = "NanoMethViz",
    c("sample1_nanopolish.tsv.gz", "sample2_nanopolish.tsv.gz"))
temp_file <- paste0(tempfile(), ".tsv.bgz")

create_tabix_file(methy_calls, temp_file)
```

---

get_exons_homo_sapiens

Get exon annotations for homo sapiens

Description

Get exon annotations for homo sapiens

Usage

```
get_exons_homo_sapiens()
```

Value

data.frame containing exons

Examples

```
h_sapiens_exons <- get_exons_homo_sapiens()
```

---

get_exons_mus_musculus

Get exon annotations for mus musculus

Description

Get exon annotations for mus musculus

Usage

```
get_exons_mus_musculus()
```

Value

data.frame containing exons

Examples

```
m_musculus_exons <- get_exons_mus_musculus()
```

load_example_nanomethresult *Load an example NanoMethResult object*

Description

Load an example NanoMethResult object

Usage

```
load_example_nanomethresult()
```

Value

a NanoMethResults object

Examples

```
nmr <- load_example_nanomethresult()
```

methy_col_names *Column names for methylation data*

Description

Column names for methylation data

Usage

```
methy_col_names()
```

Value

column names for methylation data

Examples

```
methy_col_names()
```

methy_to_bsseq *Create BSSeq object from methylation tabix file*

Description

Create BSSeq object from methylation tabix file

Usage

```
methy_to_bsseq(methy, out_folder = tempdir(), verbose = TRUE)
```

Arguments

methy	the path to the methylation tabix file.
out_folder	the folder to store intermediate files. One file is created for each sample and contains columns "chr", "pos", "total" and "methylated".
verbose	TRUE if progress messages are to be printed

Value

a BSSeq object.

Examples

```
methy <- system.file("methy_subset.tsv.bgz", package = "NanoMethViz")
bsseq <- methy_to_bsseq(methy)
```

NanoMethResult-class *Nanopore Methylation Result*

Description

A NanoMethResult object stores data used for NanoMethViz visualisation. It contains stores a path to the methylation data, sample information and optional exon information. The object is constructed using the NanoMethResult() constructor function described in "Usage".

Usage

```
NanoMethResult(methy, samples, exons = NULL)

## S4 method for signature 'NanoMethResult'
methy(object)

## S4 method for signature 'NanoMethResult'
samples(object)

## S4 method for signature 'NanoMethResult'
exons(object)
```

Arguments

methy	the path to the methylation tabix file.
samples	the data.frame of sample annotation containg at least columns sample and group.
exons	(optional) the data.frame of exon information containing at least columns gene_id, chr, strand, start, end, transcript_id and symbol.
object	the NanoMethResult object.

Value

a NanoMethResult object to be used with plotting functions

the path to the methylation data.

the sample annotation.

the exon annotation.

Functions

- NanoMethResult: Constructor
- methy,NanoMethResult-method: methylation data path getter.
- samples,NanoMethResult-method: sample annotation getter.
- exons,NanoMethResult-method: exon annotation getter.

Slots

methy the path to the methylation tabix file.

samples the data.frame of sample annotation containg at least columns sample and group.

exons the data.frame of exon information containing at least columns gene_id, chr, strand, start, end, transcript_id and symbol.

Examples

```
x <- load_example_nanomethresult()
methy(x)
```

---

plot_agg_regions *Plot aggregate regions*

Description

Plot aggregate regions

Usage

```
plot_agg_regions(
  x,
  regions,
  groups = NULL,
  flank = 2000,
  stranded = TRUE,
  span = 0.05
)
```

Arguments

x	the NanoMethResult object.
regions	a table of regions or GRanges, or a list of such objects. The table of regions must contain chr, start and end columns.
groups	if 'features' is a list, a vector of characters of the same length as the list containing names for each member.
flank	the number of flanking bases to add to each side of each region.
stranded	TRUE if negative strand features should have coordinates flipped to reflect features like transcription start sites.
span	the span for loess smoothing.

Value

a ggplot object.

---

plot_agg_regions_sample_grouped

Plot aggregate regions with grouped samples

Description

Plot aggregate regions with grouped samples

Usage

```
plot_agg_regions_sample_grouped(
  x,
  regions,
  flank = 2000,
  stranded = TRUE,
  span = 0.05
)
```

Arguments

x	the NanoMethResult object.
regions	a table of regions or GRanges, or a list of such objects. The table of regions must contain chr, start and end columns.
flank	the number of flanking bases to add to each side of each region.
stranded	TRUE if negative strand features should have coordinates flipped to reflect features like transcription start sites.
span	the span for loess smoothing.

Value

a ggplot plot object.

plot_gene *Plot gene*

Description

Plot gene

Usage

```
plot_gene(x, gene, ...)

## S4 method for signature 'NanoMethResult,character'
plot_gene(
  x,
  gene,
  window = 0.3,
  anno_regions = NULL,
  spaghetti = FALSE,
  span = NULL,
  gene_anno = TRUE
)
```

Arguments

x	the NanoMethResult object.
gene	the gene symbol for the gene to plot.
...	additional arguments
window	the size of flanking region to plot. Can be a vector of two values for left and right window size. Values indicate proportion of gene length.
anno_regions	the data.frame of regions to annotate.
spaghetti	whether or not individual reads should be shown.
span	the span for loess smoothing.
gene_anno	whether or not gene annotation tracks are plotted.

Value

a patchwork plot.

a patchwork plot.

Examples

```
nmr <- load_example_nanomethresult()
plot_gene(nmr, "Peg3")

nmr <- load_example_nanomethresult()
plot_gene(nmr, "Peg3")
```

plot_grange *Plot GRanges*

Description

Plot GRanges

Usage

```
plot_grange(x, grange, anno_regions = NULL, spaghetti = FALSE, span = NULL)
```

Arguments

x	the NanoMethResult object.
grange	the GRanges object with one entry.
anno_regions	the data.frame of regions to be annotated
spaghetti	whether or not individual reads should be shown.
span	the span for loess smoothing.

Value

a ggplot object.

a ggplot object.

Examples

```
nmr <- load_example_nanomethresult()
plot_grange(nmr, GRanges("chr7:6703892-6730431"))
```

plot_region *Plot region*

Description

Plot region

Usage

```
plot_region(x, chr, start, end, ...)

## S4 method for signature 'NanoMethResult,character,numeric,numeric'
plot_region(
  x,
  chr,
  start,
  end,
  anno_regions = NULL,
```

```
  spaghetti = FALSE,
  span = NULL
)

## S4 method for signature 'NanoMethResult,factor,numeric,numeric'
plot_region(
  x,
  chr,
  start,
  end,
  anno_regions = NULL,
  spaghetti = FALSE,
  span = NULL
)
```

Arguments

x	the NanoMethResult object
chr	the chromosome to plot
start	the start of the plotting region
end	the end of the plotting region
...	additional arguments
anno_regions	the data.frame of regions to be annotated
spaghetti	whether or not individual reads should be shown.
span	the span for loess smoothing.

Value

a ggplot object.

a ggplot object.

Examples

```
nmr <- load_example_nanomethresult()
plot_region(nmr, "chr7", 6703892, 6730431)

nmr <- load_example_nanomethresult()
plot_region(nmr, "chr7", 6703892, 6730431)
```

---

query_exons *Query exons*

Description

Query a data.frame of exons for a subset.

Usage

```
query_exons_region(exons, chr, start, end)

query_exons_gene_id(exons, gene_id)

query_exons_symbol(exons, symbol)
```

Arguments

exons	the data.frame of exons.
chr	the chromosome to query.
start	the start of the query region.
end	the end of the query region.
gene_id	the gene_id to query.
symbol	the gene_id to query.

Value

data.frame of queried exons.

Functions

- query_exons_region: Query region.
- query_exons_gene_id: Query gene ID.
- query_exons_symbol: Query gene symbol.

---

query_methy *Query methylation data*

Description

Query methylation data

Usage

```
query_methy(x, chr, start, end, simplify = TRUE)
```

Arguments

x	the path to the methylation data (tabix-bgzipped)
chr	the vector of chromosomes
start	the vector of start positions
end	the vector of end positions
simplify	whether returned results should be row-concatenated

Value

A table containing the data within the queried regions. If simplify is TRUE (default) then all data is contained within one table, otherwise it is a list of tables where each element is the data from one region.

Examples

```
nmr <- load_example_nanomethresult()
query_methy(methy(nmr), "chr7", 6703892, 6730431)
```

Index